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RAW SEQUENCE LISTING DATE: 07/24/2001
 PATENT APPLICATION: US/09/904,954 TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt
 Output Set: N:\CRF3\07242001\I904954.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: BECKMANN, M. P.
 7 CERRETTI, DOUGLAS P.
 9 (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
 10 RECEPTOR HEK
 12 (iii) NUMBER OF SEQUENCES: 4
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: IMMUNEX CORPORATION
 16 (B) STREET: 51 UNIVERSITY STREET
 17 (C) CITY: SEATTLE
 18 (D) STATE: WASHINGTON
 19 (E) COUNTRY: USA
 20 (F) ZIP: 98101
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: Apple Macintosh
 25 (C) OPERATING SYSTEM: Apple System 7.1
 26 (D) SOFTWARE: Microsoft Word for Apple, Version 5.1a
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/904,954
 C--> 30 (B) FILING DATE: 12-Jul-2001
 31 (C) CLASSIFICATION:
 41 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: 08/240,124
 35 (B) FILING DATE:
 38 (A) APPLICATION NUMBER: US 08/114,426
 39 (B) FILING DATE: 30-AUG-1993
 42 (A) APPLICATION NUMBER: US 08/109,745
 43 (B) FILING DATE: 20-AUG-1993
 45 (viii) ATTORNEY/AGENT INFORMATION:
 46 (A) NAME: SEESE, KATHRYN A.
 47 (B) REGISTRATION NUMBER: 32,172
 48 (C) REFERENCE/DOCKET NUMBER: 2814-C
 50 (ix) TELECOMMUNICATION INFORMATION:
 51 (A) TELEPHONE: (206) 587-0430
 52 (B) TELEFAX: (206) 233-0644
 53 (C) TELEX: 756822
 56 (2) INFORMATION FOR SEQ ID NO: 1:
 58 (i) SEQUENCE CHARACTERISTICS:
 59 (A) LENGTH: 1037 base pairs
 60 (B) TYPE: nucleic acid
 61 (C) STRANDEDNESS: single
 62 (D) TOPOLOGY: linear
 64 (ii) MOLECULE TYPE: cdna to mRNA
 66 (iii) HYPOTHETICAL: NO
 68 (iv) ANTI-SENSE: NO

ENTERED

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71 (vii) IMMEDIATE SOURCE:
72 (B) CLONE: hek-L A2
74 (ix) FEATURE:
75 (A) NAME/KEY: CDS
76 (B) LOCATION: 83..799
78 (ix) FEATURE:
79 (A) NAME/KEY: sig_peptide
80 (B) LOCATION: 83..139
82 (ix) FEATURE:
83 (A) NAME/KEY: mat_peptide
84 (B) LOCATION: 140..796
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
89 GGATCTTGGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTCGGGGGGC 60
91 GCGGGCGGGCG GCGGCTCCGG GG ATG GCG GCG GCT CCG CTG CTG CTG CTG CTG 112
92 Met Ala Ala Ala Pro Leu Leu Leu Leu Leu
93 -19 -15 -10
95 CTG CTC GTG CCC GTG CCG CTG CTG CCG CTG CTG GCC CAA GGG CCC GGA 160
96 Leu Leu Val Pro Val Pro Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly
97 -5 1 5
99 GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG 208
100 Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln
101 10 15 20
103 CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT 256
104 His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr
105 25 30 35
107 CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG 304
108 Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly
109 40 45 50 55
111 GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG 352
112 Ala Gly Pro Gly Pro Gly Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met
113 60 65 70
115 GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG 400
116 Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys
117 75 80 85
119 CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC 448
120 Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe
121 90 95 100
123 TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC 496
124 Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe
125 105 110 115
127 CAC GCC GGC CAC GAG TAC TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG 544
128 His Ala Gly His Glu Tyr Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu
129 120 125 130 135
131 CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC TGC GCC TCC ACA 592
132 His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr
133 140 145 150
135 TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG 640
136 Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met
137 155 160 165

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139 GGC CCC AAT GTG AAG ATC AAC GTG CTG GAA GAC TTT GAG GGA GAG AAC 688
140 Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn
141 170 175 180
143 CCT CAG GTG CCC AAG CTT GAG AAG AGC ATC AGC GGG ACC AGC CCC AAA 736
144 Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys
145 185 190 195
147 CGG GAA CAC CTG CCC CTG GCC GTG GGC ATC GCC TTC TTC CTC ATG ACG 784
148 Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr
149 200 205 210 215
151 TTC TTG GCC TCC TAGCTCTGCC CCCTCCCCTG GGGGGGGAGA GATGGGGCGG 836
152 Phe Leu Ala Ser
W--> 153 220
155 GGCTTGAAG GAGCAGGGAG CCTTTGGCCT CTCCAAGGGA AGCCTAGTGG GCCTAGACCC 896
157 CTCCTCCCAT GGCTAGAAGT GGGGCCTGCA CCATACATCT GTGTCCGCC CCTCTACCC 956
159 TTCCCCCAG GTAGGGCACT GTAGTGGACC AAGCACGGGG ACAGCCATGG GTCCCGAGCA 1016
161 GGTCGTCTCG TTCCAAGATC C 1037
164 (2) INFORMATION FOR SEQ ID NO: 2:
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 238 amino acids
168 (B) TYPE: amino acid
169 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: protein
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
175 Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Leu Val Pro Val Pro
176 -19 -15 -10 -5
178 Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg
179 1 5 10
181 His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly
182 15 20 25
184 Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro
185 30 35 40 45
187 His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly
188 50 55 60
190 Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr
191 65 70 75
193 Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg
194 80 85 90
196 Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg
197 95 100 105
199 Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr
200 110 115 120 125
202 Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg
203 130 135 140
205 Met Lys Val Phe Val Cys Cys Ala Ser Thr Ser His Ser Gly Glu Lys
206 145 150 155
208 Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys Ile
209 160 165 170
211 Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys Leu
212 175 180 185

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214 Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys Arg Glu His Leu Pro Leu
215 190                               195                               200                               205
217 Ala Val Gly Ile Ala Phe Phe Leu Met Thr Phe Leu Ala Ser
218                               210                               215
221 (2) INFORMATION FOR SEQ ID NO: 3:
222   (i) SEQUENCE CHARACTERISTICS:
223       (A) LENGTH: 636 base pairs
224       (B) TYPE: nucleic acid
225       (C) STRANDEDNESS: single
226       (D) TOPOLOGY: linear
227   (ii) MOLECULE TYPE: cDNA to mRNA
231   (iii) HYPOTHETICAL: NO
233   (iv) ANTI-SENSE: NO
236   (vii) IMMEDIATE SOURCE:
237       (B) CLONE: hek-L C6
239   (ix) FEATURE:
240       (A) NAME/KEY: mat_peptide
241       (B) LOCATION: 94..630
243   (ix) FEATURE:
244       (A) NAME/KEY: CDS
245       (B) LOCATION: 28..633
247   (ix) FEATURE:
248       (A) NAME/KEY: sig_peptide
249       (B) LOCATION: 28..93
252   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
254 GCCAGACCAA ACCGGACCTC GGGGGCG ATG CGG CTG CTG CCC CTG CTG CGG           51
255                               Met Arg Leu Leu Pro Leu Leu Arg
256                               -22   -20                               -15
258 ACT GTC CTC TGG GCC GCG TTC CTC GGC TCC CCT CTG CGC GGG GGC TCC           99
259 Thr Val Leu Trp Ala Ala Phe Leu Gly Ser Pro Leu Arg Gly Gly Ser
260                               -10                               -5                               1
262 AGC CTC CGC CAC GTA GTC TAC TGG AAC TCC AGT AAC CCC AGG TTG CTT           147
263 Ser Leu Arg His Val Val Tyr Trp Asn Ser Ser Asn Pro Arg Leu Leu
264                               5                               10                               15
266 CGA GGA GAC GCC GTG GTG GAG CTG GGC CTC AAC GAT TAC CTA GAC ATT           195
267 Arg Gly Asp Ala Val Val Glu Leu Gly Leu Asn Asp Tyr Leu Asp Ile
268                               20                               25                               30
270 GTC TGC CCC CAC TAC GAA GGC CCA GGG CCC CCT GAG GGC CCC GAG ACG           243
271 Val Cys Pro His Tyr Glu Gly Pro Gly Pro Pro Glu Gly Pro Glu Thr
272 35                               40                               45                               50
274 TTT GCT TTG TAC ATG GTG GAC TGG CCA GGC TAT GAG TCC TGC CAG GCA           291
275 Phe Ala Leu Tyr Met Val Asp Trp Pro Gly Tyr Glu Ser Cys Gln Ala
276                               55                               60                               65
278 GAG GGC CCC CGG GCC TAC AAG CGC TGG GTG TGC TCC CTG CCC TTT GGC           339
279 Glu Gly Pro Arg Ala Tyr Lys Arg Trp Val Cys Ser Leu Pro Phe Gly
280                               70                               75                               80
282 CAT GTT CAA TTC TCA GAG AAG ATT CAG CGC TTC ACA CCT TTC TCC CTC           387
283 His Val Gln Phe Ser Glu Lys Ile Gln Arg Phe Thr Pro Phe Ser Leu
284                               85                               90                               95

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286 GGC TTT GAG TTC TTA CCT GGA GAG ACT TAC TAC TAC ATC TCG GTG CCC      435
287 Gly Phe Glu Phe Leu Pro Gly Glu Thr Tyr Tyr Tyr Ile Ser Val Pro
288      100                      105                      110
290 ACT CCA GAG AGT TCT GGC CAG TGC TTG AGG CTC CAG GTG TCT GTC TGC      483
291 Thr Pro Glu Ser Ser Gly Gln Cys Leu Arg Leu Gln Val Ser Val Cys
292 115                      120                      125                      130
294 TGC AAG GAG AGG AAG TCT GAG TCA GCC CAT CCT GTT GGG AGC CCT GGA      531
295 Cys Lys Glu Arg Lys Ser Glu Ser Ala His Pro Val Gly Ser Pro Gly
296                      135                      140                      145
298 GAG AGT GGC ACA TCA GGG TGG CGA GGG GGG GAC ACT CCC AGC CCC CTC      579
299 Glu Ser Gly Thr Ser Gly Trp Arg Gly Gly Asp Thr Pro Ser Pro Leu
300                      150                      155                      160
302 TGT CTC TTG CTA TTA CTG CTG CTT CTG ATT CTT CGT CTT CTG CGA ATT      627
303 Cys Leu Leu Leu Leu Leu Leu Leu Leu Ile Leu Arg Leu Leu Arg Ile
304                      165                      170                      175
306 CTG TGAGCC
307 Leu
W--> 308      180
312 (2) INFORMATION FOR SEQ ID NO: 4:
314 (i) SEQUENCE CHARACTERISTICS:
315 (A) LENGTH: 201 amino acids
316 (B) TYPE: amino acid
317 (D) TOPOLOGY: linear
319 (ii) MOLECULE TYPE: protein
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
323 Met Arg Leu Leu Pro Leu Leu Arg Thr Val Leu Trp Ala Ala Phe Leu
324 -22 -20 -15 -10
326 Gly Ser Pro Leu Arg Gly Gly Ser Ser Leu Arg His Val Val Tyr Trp
327 -5 1 5 10
329 Asn Ser Ser Asn Pro Arg Leu Leu Arg Gly Asp Ala Val Val Glu Leu
330 15 20 25
332 Gly Leu Asn Asp Tyr Leu Asp Ile Val Cys Pro His Tyr Glu Gly Pro
333 30 35 40
335 Gly Pro Pro Glu Gly Pro Glu Thr Phe Ala Leu Tyr Met Val Asp Trp
336 45 50 55
338 Pro Gly Tyr Glu Ser Cys Gln Ala Glu Gly Pro Arg Ala Tyr Lys Arg
339 60 65 70
341 Trp Val Cys Ser Leu Pro Phe Gly His Val Gln Phe Ser Glu Lys Ile
342 75 80 85 90
344 Gln Arg Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Leu Pro Gly Glu
345 95 100 105
347 Thr Tyr Tyr Tyr Ile Ser Val Pro Thr Pro Glu Ser Ser Gly Gln Cys
348 110 115 120
350 Leu Arg Leu Gln Val Ser Val Cys Cys Lys Glu Arg Lys Ser Glu Ser
351 125 130 135
353 Ala His Pro Val Gly Ser Pro Gly Glu Ser Gly Thr Ser Gly Trp Arg
354 140 145 150
356 Gly Gly Asp Thr Pro Ser Pro Leu Cys Leu Leu Leu Leu Leu Leu
357 155 160 165 170

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:59

Input Set : N:\Crf3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3